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Leu Lys Ala Gly Thr Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp

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cgc cgc atg gcc aac aca gcc tcc gcc gct gcc gga aac cca ccg gcc 193

Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly

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gag gcc tta aga aac ctg ctt ctg aac aac cac gac gtc acg ttc gtc 337

Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn His Asp Val Thr Phe Val

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gtc tac tcc cac ctg ttt gca tgg gcg gcg gag gtg gcg cgt gag tcc 385

Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser

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Gln Val Pro Ser Ala Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys	
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 Tyr Ala Trp Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Ala Gly Asn  
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 Leu Lys Pro Gly Gly Asp Gly Lys Arg Tyr Met Ser Glu Met Lys Ala  
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 Arg Gly Ser Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn Asp Asp Val  
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 Arg Leu Ser His Val Pro Thr Ala Leu Leu Trp Val Glu Pro Ala Thr  
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 Val Leu Cys Ile Tyr His Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile  
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 Asp Ala Gly Ser Asn Glu Ile Gln Leu Pro Arg Leu Pro Ser Leu Glu  
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 Gln Arg Ser Leu Pro Thr Phe Leu Leu Pro Ala Thr Pro Glu Arg Phe  
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 Trp Phe Asp Gln Thr Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly  
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 Glu Ile Glu Arg Cys Val Glu Met Val Met Asp Gly Gly Asp Lys Thr  
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 Lys Leu Val Arg Glu Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Gln  
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 Ala Trp Arg Arg Met Ser Arg Thr Ala Ala Gly Ser Asn Gly Leu Ile  
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Val Ala Arg Glu Phe His Leu Arg Ser Ala Leu Leu Trp Ile Glu Pro	
125 130 135	
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205 210 215	
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Val Val Gly Ile  
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Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Met Ile Glu	
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 Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro Leu  
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 Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr  
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gct ctc ctg ggg ttc gtg gac gtc cac ggc aat tat ctt gtt aat aaa	587
Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn Lys	
85 90 95	
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Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys Trp	
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Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr Lys	
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Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly Leu	
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ctc ctc gtg ctt ctt tcc gac tca ggg gtc act gct gct ggt tcg aat	779
Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser Asn	
150 155 160	
cct ctt ttg ggt gat ttt ctt gtc ata aca ggc tct att ttg ttc aca	827
Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe Thr	
165 170 175	
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Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg Ile	
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gaa gta gta gca atg atc ggt gta ttt ggt atg ctc atc agt gca acc	923
Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala Thr	
195 200 205 210	
gag att act gtg ctg gag agg aat gcc ctc tca tca atg cag tgg tct	971
Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp Ser	
215 220 225	
act gga ctt ttg gca gcc tat gtt gtt tat gca ctg tcc agc ttc ctc	1019
Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe Leu	
230 235 240	
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Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala Phe	
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Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile Arg	
260 265 270	

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Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys Asp  
295 300 305  
cct aac aat acg aga gcc ctt gag aat gga aac ttg gat cat gaa tat 1259  
Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu Tyr  
310 315 320  
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Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro  
325 330 335  
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Met Val Gln Pro His Val  
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Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln  
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Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr  
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Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala  
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Pro	Lys	Gly	Leu	Asn	Phe	Ile	Pro	Phe	Ser	Asp	Gly	Phe	Asp	Glu	Gly	
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Phe	Asp	His	Ser	Lys	Asp	Pro	Val	Phe	Tyr	Met	Ser	Gln	Leu	Arg	Lys	
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tgt	gga	agt	gaa	act	gtc	aaa	aaa	ata	att	ctc	act	tgc	tct	gaa	aat	646
Cys	Gly	Ser	Glu	Thr	Val	Lys	Lys	Ile	Ile	Leu	Thr	Cys	Ser	Glu	Asn	
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Gly	Gln	Pro	Ile	Thr	Cys	Leu	Leu	Tyr	Ser	Ile	Phe	Leu	Pro	Trp	Ala	
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gca	gag	gta	gca	cgt	gaa	gtt	cac	atc	cct	tct	gct	ctt	ctt	tgg	agt	742
Ala	Glu	Val	Ala	Arg	Glu	Val	His	Ile	Pro	Ser	Ala	Leu	Leu	Trp	Ser	
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Gln	Pro	Ala	Thr	Ile	Leu	Asp	Ile	Tyr	Tyr	Phe	Asn	Phe	His	Gly	Tyr	
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Glu	Lys	Ala	Met	Ala	Asn	Glu	Ser	Asn	Asp	Pro	Asn	Trp	Ser	Ile	Gln	
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ctt	ccc	ggg	ctt	cca	cta	ctg	gaa	act	cga	gat	ctt	cct	tca	ttt	tta	886
Leu	Pro	Gly	Leu	Pro	Leu	Leu	Glu	Thr	Arg	Asp	Leu	Pro	Ser	Phe	Leu	
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Leu	Pro	Tyr	Gly	Ala	Lys	Gly	Ser	Leu	Arg	Val	Ala	Leu	Pro	Pro	Phe	
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Lys	Glu	Leu	Ile	Asp	Thr	Leu	Asp	Ala	Glu	Thr	Thr	Pro	Lys	Ile	Leu	
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gtg	aat	aca	ttt	gat	gaa	tta	gag	cct	gag	gca	ctc	aat	gca	att	gaa	1030
Val	Asn	Thr	Phe	Asp	Glu	Leu	Glu	Pro	Glu	Ala	Leu	Asn	Ala	Ile	Glu	
215				220				225					230			
ggc	tat	aag	ttt	tat	gga	att	gga	ccg	ttg	att	cct	tct	gct	ttc	ttg	1078
Gly	Tyr	Lys	Phe	Tyr	Gly	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu	
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Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe Gly Gly Asp Leu Phe Gln	
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aat tca aat gac tat atg gaa tgg tta aac tca aag cca aat tca tca	1174
Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn Ser Lys Pro Asn Ser Ser	
265 270 275	
gtt gtt tat ata tct ttt ggg agt cta atg aat cca tct att agc caa	1222
Val Val Tyr Ile Ser Phe Gly Ser Leu Met Asn Pro Ser Ile Ser Gln	
280 285 290	
atg gag gag ata tca aaa ggg ttg ata gac ata gga agg ccg ttt tta	1270
Met Glu Glu Ile Ser Lys Gly Leu Ile Asp Ile Gly Arg Pro Phe Leu	
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Trp Val Ile Lys Glu Asn Glu Lys Gly Lys Glu Glu Glu Asn Lys Lys	
315 320 325	
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Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile Gly Lys Ile Val Pro Trp	
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Cys Ser Gln Leu Glu Val Leu Lys His Pro Ser Leu Gly Cys Phe Val	
345 350 355	
tct cat tgt gga tgg aat tca gcc tta gag agt tta gct tgt gga gtg	1462
Ser His Cys Gly Trp Asn Ser Ala Leu Glu Ser Leu Ala Cys Gly Val	
360 365 370	
cca gtt gtg gca ttt cct caa tgg aca gat caa atg aca aat gcc aaa	1510
Pro Val Val Ala Phe Pro Gln Trp Thr Asp Gln Met Thr Asn Ala Lys	
375 380 385 390	
caa gtt gaa gat gtg tgg aaa agt gga gta aga gtg aga ata aat gaa	1558
Gln Val Glu Asp Val Trp Lys Ser Gly Val Arg Val Arg Ile Asn Glu	
395 400 405	
gat ggt gtt gtt gaa agt gag gaa atc aaa agg tgt att gaa ttg gta	1606
Asp Gly Val Val Glu Ser Glu Glu Ile Lys Arg Cys Ile Glu Leu Val	
410 415 420	
atg gat gga gga gag aaa ggg gaa gaa ttg aga aag aat gct aag aaa	1654
Met Asp Gly Gly Glu Lys Gly Glu Glu Leu Arg Lys Asn Ala Lys Lys	
425 430 435	



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 Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His  
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 aag aat tta aag gct ttt att gat gat gtt gcc aaa ggg ttt taatatttac 1754  
 Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe  
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 Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala  
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 Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Cys Gly Asp Gly Lys  
 65 70 75 80  
 Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn  
 85 90 95  
 Leu Leu Leu Asn Asn His Asp Val Thr Phe Val Val Tyr Ser His Leu  
 100 105 110  
 Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser Gln Val Pro Ser Ala  
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 Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr Tyr Phe Tyr  
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Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly Ser Asp Glu Ile Gln			
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Leu Pro Arg Leu Pro Pro Leu Glu Gln Arg Ser Leu Pro Thr Phe Leu			
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Leu Pro Glu Thr Pro Glu Arg Phe Arg Leu Met Met Lys Glu Lys Leu			
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Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val Leu Val Asn Thr Phe			
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Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile Asp Arg Tyr Glu Leu			
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Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu Asp Gly Gly Asp			
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Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe Glu Lys Ser Glu Glu			
	245	250	255
Asn Asn Cys Val Glu Trp Leu Asp Thr Lys Pro Lys Ser Ser Val Val			
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Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro Lys Ala Gln Met Glu			
	275	280	285
Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg Pro Phe Leu Trp Met			
	290	295	300
Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu Glu Glu Glu Glu Leu			
305	310	315	320
Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys Ile Val Ser Trp Cys			
	325	330	335
Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu Gly Cys Phe Val Thr			
	340	345	350
His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu Ser Cys Gly Val Pro			
	355	360	365
Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr Thr Asn Ala Lys Leu			
	370	375	380
Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val Arg Met Asn Glu Gly			
385	390	395	400
Gly Gly Val Asp Gly Ser Glu Ile Glu Arg Cys Val Glu Met Val Met			
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Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu Asn Ala Ile Lys Trp  
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 Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp Gly Ser Ser Leu Lys  
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 Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn  
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 Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala  
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 Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Gly Gly Asp Gly Lys  
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 Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn  
                                   85                                  90                                  95  
 Leu Leu Leu Asn Asn Asp Asp Val Thr Phe Val Val Tyr Ser His Leu  
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 Phe Ala Trp Ala Ala Glu Val Ala Arg Leu Ser His Val Pro Thr Ala  
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 Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr His Phe Tyr  
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 Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly Ser Asn Glu Ile Gln  
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 Leu Pro Arg Leu Pro Ser Leu Glu Gln Arg Ser Leu Pro Thr Phe Leu  
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 Leu Pro Ala Thr Pro Glu Arg Phe Arg Leu Met Met Lys Glu Lys Leu  
                   180                                  185                                  190

Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val Leu Val Asn Thr Phe			
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Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile Asp Arg Tyr Glu Leu			
210	215	220	
Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu Asp Gly Glu Asp			
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Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe Glu Lys Ser Glu Glu			
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Asn Asn Cys Val Glu Trp Leu Asn Ser Lys Pro Lys Ser Ser Val Val			
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Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro Lys Ala Gln Met Glu			
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Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg Pro Phe Leu Trp Met			
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Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu Glu Glu Glu Glu			
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Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys Ile Val Ser			
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Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu Gly Cys Phe			
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Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu Ser Cys Gly			
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Ile Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr Thr Asn Ala			
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Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val Arg Met Asn			
385	390	395	400
Glu Gly Gly Gly Val Asp Gly Cys Glu Ile Glu Arg Cys Val Glu Met			
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Val Met Asp Gly Gly Asp Lys Thr Lys Leu Val Arg Glu Asn Ala Ile			
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Gln	Val	Thr	Phe	Phe	Thr	Ser	Val	Tyr	Ala	Trp	Arg	Arg	Met	Ser	Arg
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Thr	Ala	Ala	Gly	Ser	Asn	Gly	Leu	Ile	Asn	Phe	Val	Ser	Phe	Ser	Asp
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Gly	Tyr	Asp	Asp	Gly	Leu	Gln	Pro	Gly	Asp	Asp	Gly	Lys	Asn	Tyr	Met
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Ser	Glu	Met	Lys	Ser	Arg	Gly	Ile	Lys	Ala	Leu	Ser	Asp	Thr	Leu	Ala
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Ala	Asn	Asn	Val	Asp	Gln	Lys	Ser	Ser	Lys	Ile	Thr	Phe	Val	Val	Tyr
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Ser	His	Leu	Phe	Ala	Trp	Ala	Ala	Lys	Val	Ala	Arg	Glu	Phe	His	Leu
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Arg	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala	Thr	Val	Leu	Asp	Ile	Phe
	130					135					140				
Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ser	Asp	Glu	Ile	Asp	Ala	Gly	Ser	Asp
145					150				155					160	
Ala	Ile	His	Leu	Pro	Gly	Gly	Leu	Pro	Val	Leu	Ala	Gln	Arg	Asp	Leu
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Pro	Ser	Phe	Leu	Leu	Pro	Ser	Thr	His	Glu	Arg	Phe	Arg	Ser	Leu	Met
		180					185					190			
Lys	Glu	Lys	Leu	Glu	Thr	Leu	Glu	Gly	Glu	Glu	Lys	Pro	Lys	Val	Leu
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Val	Asn	Ser	Phe	Asp	Ala	Leu	Glu	Pro	Asp	Ala	Leu	Lys	Ala	Ile	Asp
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Lys	Tyr	Glu	Met	Ile	Ala	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu
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Asp	Gly	Lys	Asp	Pro	Ser	Asp	Arg	Ser	Phe	Gly	Gly	Asp	Leu	Phe	Glu
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Lys	Gly	Ser	Asn	Asp	Asp	Asp	Cys	Leu	Glu	Trp	Leu	Ser	Thr	Asn	Pro
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Arg	Ser	Ser	Val	Val	Tyr	Val	Ser	Phe	Gly	Ser	Phe	Val	Asn	Thr	Thr			
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Lys	Ser	Gln	Met	Glu	Glu	Ile	Ala	Arg	Gly	Leu	Leu	Asp	Cys	Gly	Arg			
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Pro	Phe	Leu	Trp	Val	Val	Arg	Val	Asn	Glu	Gly	Glu	Glu	Val	Leu	Ile			
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Ser	Cys	Met	Glu	Glu	Leu	Lys	Arg	Val	Gly	Lys	Ile	Val	Ser	Trp	Cys			
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Ser	Gln	Leu	Glu	Val	Leu	Thr	His	Pro	Ser	Leu	Gly	Cys	Phe	Val	Thr			
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His	Cys	Gly	Trp	Asn	Ser	Thr	Leu	Glu	Ser	Ile	Ser	Phe	Gly	Val	Pro			
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Met	Val	Ala	Phe	Pro	Gln	Trp	Phe	Asp	Gln	Gly	Thr	Asn	Ala	Lys	Leu			
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Met	Glu	Asp	Val	Trp	Arg	Thr	Gly	Val	Arg	Val	Arg	Ala	Asn	Glu	Glu			
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Gly	Ser	Val	Val	Asp	Gly	Asp	Glu	Ile	Arg	Arg	Cys	Ile	Glu	Glu	Val			
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Met	Asp	Gly	Gly	Glu	Lys	Ser	Arg	Lys	Leu	Arg	Glu	Ser	Ala	Gly	Lys			
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Trp	Lys	Asp	Leu	Ala	Arg	Lys	Ala	Met	Glu	Glu	Asp	Gly	Ser	Ser	Val			
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His	Ile	Asn	Pro	Ser	Leu	Glu	Phe	Ala	Lys	Arg	Leu	Leu	Asn	Thr	Gly			
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Tyr	Val	Asp	Gln	Val	Thr	Phe	Phe	Thr	Ser	Val	Tyr	Ala	Leu	Arg	Arg			
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Met	Arg	Phe	Glu	Thr	Asp	Pro	Ser	Ser	Arg	Ile	Asp	Phe	Val	Ala	Xaa			
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Ala	Arg	Glu	Val	Asp	Val	Pro	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala			
		130					135					140						
Thr	Val	Phe	Asp	Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp			
	145				150					155				160				
Ile	Asp	Ala	Gly	Ser	Asp	Gln	Ile	Gln	Leu	Pro	Asn	Leu	Pro	Gln	Leu			
			165					170						175				
Ser	Lys	Gln	Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg			
			180					185					190					
Phe	Arg	Thr	Leu	Met	Lys	Glu	Lys	Phe	Asp	Thr	Leu	Asp	Lys	Glu	Pro			
		195					200					205						
Lys	Ala	Lys	Val	Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Thr	Glu	Gln			
	210					215					220							
Leu	Lys	Ala	Ile	Asp	Arg	Tyr	Glu	Leu	Ile	Ser	Ile	Gly	Pro	Leu	Ile			
	225				230					235				240				
Pro	Ser	Ser	Ile	Phe	Ser	Asp	Gly	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys			
			245					250						255				
Ser	Tyr	Gly	Gly	Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp			
		260					265						270					
Trp	Leu	Asn	Ser	Lys	Pro	Glu	Ser	Ser	Val	Val	Tyr	Val	Ser	Phe	Gly			
		275					280						285					

Ser Leu Leu Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly  
 290 295 300  
 Leu Ser Asp Thr Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu  
 305 310 315 320  
 Glu Gly Asp Glu Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser  
 325 330 335  
 Phe Phe Asp Arg His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp  
 340 345 350  
 Cys Ser Gln Leu Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val  
 355 360 365  
 Thr His Cys Gly Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val  
 370 375 380  
 Pro Val Val Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys  
 385 390 395 400  
 Met Ile Glu Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu  
 405 410 415  
 Glu Gly Gly Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu  
 420 425 430  
 Val Ile Lys Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly  
 435 440 445  
 Leu Ala Lys Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn  
 450 455 460  
 Leu Lys Asn Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser  
 465 470 475 478  
 <210> 11  
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 <212> PRT  
 <213> *Perilla frutescens*  
 <400> 11  
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 1 5 10 15  
 Arg Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu  
 20 25 30  
 Ala Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala  
 35 40 45



Pro Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr  
 50 55 60  
 Gly Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr  
 65 70 75 80  
 Trp Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val  
 85 90 95  
 Asn Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp  
 100 105 110  
 Cys Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly  
 115 120 125  
 Thr Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly  
 130 135 140  
 Gly Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly  
 145 150 155 160  
 Ser Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu  
 165 170 175  
 Phe Thr Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp  
 180 185 190  
 Arg Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser  
 195 200 205  
 Ala Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln  
 210 215 220  
 Trp Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser  
 225 230 235 240  
 Phe Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala  
 245 250 255  
 Ala Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala  
 260 265 270  
 Ile Arg Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu  
 275 280 285  
 Ala Phe Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu  
 290 295 300  
 Lys Asp Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His  
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 Glu Tyr Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro  
 325 330 335  
 <210> 12  
 <211> 468

<212> PRT

<213> Petunia hybrida

<400> 12

Met Val Gln Pro His Val Ile Leu Thr Thr Phe Pro Ala Gln Gly His  
1 5 10 15  
Ile Asn Pro Ala Leu Gln Phe Ala Lys Asn Leu Val Lys Met Gly Ile  
20 25 30  
Glu Val Thr Phe Ser Thr Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu  
35 40 45  
Lys Ser Ile Leu Asn Ala Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser  
50 55 60  
Asp Gly Phe Asp Glu Gly Phe Asp His Ser Lys Asp Pro Val Phe Tyr  
65 70 75 80  
Met Ser Gln Leu Arg Lys Cys Gly Ser Glu Thr Val Lys Lys Ile Ile  
85 90 95  
Leu Thr Cys Ser Glu Asn Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser  
100 105 110  
Ile Phe Leu Pro Trp Ala Ala Glu Val Ala Arg Glu Val His Ile Pro  
115 120 125  
Ser Ala Leu Leu Trp Ser Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr  
130 135 140  
Phe Asn Phe His Gly Tyr Glu Lys Ala Met Ala Asn Glu Ser Asn Asp  
145 150 155 160  
Pro Asn Trp Ser Ile Gln Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg  
165 170 175  
Asp Leu Pro Ser Phe Leu Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg  
180 185 190  
Val Ala Leu Pro Pro Phe Lys Glu Leu Ile Asp Thr Leu Asp Ala Glu  
195 200 205  
Thr Thr Pro Lys Ile Leu Val Asn Thr Phe Asp Glu Leu Glu Pro Glu  
210 215 220  
Ala Leu Asn Ala Ile Glu Gly Tyr Lys Phe Tyr Gly Ile Gly Pro Leu  
225 230 235 240  
Ile Pro Ser Ala Phe Leu Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe  
245 250 255  
Gly Gly Asp Leu Phe Gln Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn  
260 265 270

Ser Lys Pro Asn Ser Ser Val Val Tyr Ile Ser Phe Gly Ser Leu Met			
275	280	285	
Asn Pro Ser Ile Ser Gln Met Glu Glu Ile Ser Lys Gly Leu Ile Asp			
290	295	300	
Ile Gly Arg Pro Phe Leu Trp Val Ile Lys Glu Asn Glu Lys Gly Lys			
305	310	315	320
Glu Glu Glu Asn Lys Lys Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile			
325	330	335	
Gly Lys Ile Val Pro Trp Cys Ser Gln Leu Glu Val Leu Lys His Pro			
340	345	350	
Ser Leu Gly Cys Phe Val Ser His Cys Gly Trp Asn Ser Ala Leu Glu			
355	360	365	
Ser Leu Ala Cys Gly Val Pro Val Val Ala Phe Pro Gln Trp Thr Asp			
370	375	380	
Gln Met Thr Asn Ala Lys Gln Val Glu Asp Val Trp Lys Ser Gly Val			
385	390	395	400
Arg Val Arg Ile Asn Glu Asp Gly Val Val Glu Ser Glu Glu Ile Lys			
405	410	415	
Arg Cys Ile Glu Leu Val Met Asp Gly Gly Glu Lys Gly Glu Glu Leu			
420	425	430	
Arg Lys Asn Ala Lys Lys Trp Lys Glu Leu Ala Arg Glu Ala Val Lys			
435	440	445	
Glu Gly Gly Ser Ser His Lys Asn Leu Lys Ala Phe Ile Asp Asp Val			
450	455	460	
Ala Lys Gly Phe			
465	468		

# Sequence

Sequence ID No.: 1

Sequence length: 1507

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: *Perilla* (*Perilla frutescens*)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p3R4

Sequence:

GAAAAATTC	ACAAAA	ATG	GTC	CGC	CGC	CGC	GTG	CTG	CTA	GCA	ACG	TTT	49
Met Val Arg Arg Arg Val Leu Leu Ala Thr Phe													
1			5			10							
CCT	GCG	CAA	GGC	CAC	ATA	AAT	CCC	GCC	CTC	CAA	TTC	GCC	97
Pro	Ala	Gln	Gly	His	Ile	Asn	Pro	Ala	Leu	Gln	Phe	Ala	
15			20			25							
CTA	AAA	GCC	GGC	ACT	GAC	GTC	ACA	TTT	TTC	ACG	AGC	GTT	145
Leu	Lys	Ala	Gly	Thr	Asp	Val	Thr	Phe	Phe	Thr	Ser	Val	
30			35			40							
CGC	CGC	ATG	GCC	AAC	ACA	GCC	TCC	GCC	GCT	GCC	GGA	AAC	193
Arg	Arg	Met	Ala	Asn	Thr	Ala	Ser	Ala	Ala	Ala	Gly	Asn	
45			50			55							
CTC	GAC	TTC	GTG	GCG	TTC	TCC	GAC	GGC	TAC	GAC	GAC	GGG	241
Leu	Asp	Phe	Val	Ala	Phe	Ser	Asp	Gly	Tyr	Asp	Asp	Gly	
60			65			70			75				
TGC	GGC	GAC	GGG	AAG	CGC	TAC	ATG	TCC	GAG	ATG	AAA	GCC	289
Cys	Gly	Asp	Gly	Lys	Arg	Tyr	Met	Ser	Glu	Met	Lys	Ala	
80			85			90							
GAG	GCC	TTA	AGA	AAC	CTC	CTT	CTC	AAC	AAC	CAC	GAC	GTC	337
Glu	Ala	Leu	Arg	Asn	Leu	Leu	Leu	Asn	Asn	His	Asp	Val	
95			100			105							

GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG CGT GAG TCC	385
Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser	
110 115 120	
CAG GTC CCG AGC GCC CTT CTC TGG GTC GAG CCC GCC ACC GTG CTG TGC	433
Gln Val Pro Ser Ala Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys	
125 130 135	
ATA TAT TAC TTC TAC TTC AAC GGC TAC GCA GAC GAG ATC GAC GCC GGT	481
Ile Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly	
140 145 150 155	
TCC GAC GAA ATT CAG CTC CCT CGG CTT CCA CCC CTG GAG CAG CGC AGT	529
Ser Asp Glu Ile Gln Leu Pro Arg Leu Pro Pro Leu Glu Gln Arg Ser	
160 165 170	
CTT CCG ACC TTT CTG CTG CCG GAG ACA CCG GAG AGA TTC CGG TTG ATG	577
Leu Pro Thr Phe Leu Leu Pro Glu Thr Pro Glu Arg Phe Arg Leu Met	
175 180 185	
ATG AAG GAG AAG CTG GAA ACT TTA GAC GGT GAA GAG AAG GCG AAA GTG	625
Met Lys Glu Lys Leu Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val	
190 195 200	
TTG GTG AAC ACG TTT GAT GCG TTG GAG CCC GAT GCA CTC ACG GCT ATT	673
Leu Val Asn Thr Phe Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile	
205 210 215	
GAT AGG TAT GAG TTG ATC GGG ATC GGG CCG TTG ATT CCC TCC GCC TTC	721
Asp Arg Tyr Glu Leu Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe	
220 225 230 235	
TTG GAC GGC GGA GAT CCC TCC GAA ACG TCT TAC GGC GGC GAT CTT TTC	769
Leu Asp Gly Gly Asp Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe	
240 245 250	
GAA AAA TCG GAG GAG AAT AAC TGC GTG GAG TGG TTG GAC ACG AAG CCG	817
Glu Lys Ser Glu Glu Asn Asn Cys Val Glu Trp Leu Asp Thr Lys Pro	
255 260 265	
AAA TCT TCG GTG GTG TAT GTG TCG TTT GGG AGC GTT TTG AGG TTT CCA	865
Lys Ser Ser Val Val Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro	
270 275 280	
AAG GCA CAA ATG GAA GAG ATT GGG AAA GGG CTA TTA GCC TGC GGA AGG	913
Lys Ala Gln Met Glu Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg	
285 290 295	

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CCG TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC GGC GAA GAA      961
Pro Phe Leu Trp Met Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu
300                      305                      310                      315
GAA GAA GAA GAG TTG AGT TGC ATT GGG GAA TTG AAA AAA ATG GGG AAA      1009
Glu Glu Glu Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys
                      320                      325                      330
ATA GTT TCG TGG TGC TCG CAG TTG GAG GTT CTG GCG CAC CCT GCG TTG      1057
Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu
                      335                      340                      345
GGA TGT TTC GTG ACG CAT TGT GGG TGG AAC TCG GCT GTG GAG AGC TTG      1105
Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu
                      350                      355                      360
AGT TGC GGG GTT CCG GTG GTG GCG GTG CCG CAG TGG TTT GAT CAG ACG      1153
Ser Cys Gly Val Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr
                      365                      370                      375
ACG AAT GCG AAG CTG ATT GAG GAT GCG TGG GGG ACA GGG GTG AGA GTG      1201
Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val
380                      385                      390                      395
AGA ATG AAT GAA GGG GGT GGG GTT GAT GGA TCT GAG ATA GAG AGG TGT      1249
Arg Met Asn Glu Gly Gly Gly Val Asp Gly Ser Glu Ile Glu Arg Cys
                      400                      405                      410
GTG GAG ATG GTG ATG GAT GGG GGT GAG AAG AGC AAA CTA GTG AGA GAA      1297
Val Glu Met Val Met Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu
                      415                      420                      425
AAT GCC ATA AAA TGG AAG ACT TTG GCC AGA GAA GCC ATG GGA GAG GAT      1345
Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp
                      430                      435                      440
GGA TCT TCA CTC AAG AAT CTC AAC GCC TTT CTT CAT CAA GTT GCA CGT      1393
Gly Ser Ser Leu Lys Asn Leu Asn Ala Phe Leu His Gln Val Ala Arg
                      445                      450                      455
GCT TAATACACAA AATGGCTTTC CACTTTTAAT CTACTCAAAC ACCGGTTCAA      1446
Ala
460                                                                1507
ATAAATATCC CCTTCCAATT CTTTCTATTT CACTATCACA TTTATAATTT TAGTAACAAA 1506
A

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Sequence ID No.: 2  
Sequence length: 1470

CCG TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC GGC GAA GAA

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Perilla (Perilla frutescens)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p3R6

Sequence:

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ACCAAACCAA AACAAAATTT CCACAAAA ATG GTC CGC CGC CGC GTG CTG CTA      48
                               Met Val Arg Arg Arg Val Leu Leu
                               1           5

GCA ACG TTT CCG GCG CAA GGC CAC ATA AAT CCC GCC CTC CAA TTC GCC      96
Ala Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala
    10           15           20

AAG AGA CTC CTA AAA GCC GGC ACT GAC GTC ACG TTT TTC ACG AGC GTT      144
Lys Arg Leu Leu Lys Ala Gly Thr Asp Val Thr Phe Phe Thr Ser Val
    25           30           35           40

TAT GCA TGG CGC CGC ATG GCC AAC ACA GCC TCC GCC GCT GCC GGA AAC      192
Tyr Ala Trp Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Ala Gly Asn
           45           50           55

CCA CCG GGC CTC GAC TTC GTG GCG TTC TCC GAC GGC TAC GAC GAC GGG      240
Pro Pro Gly Leu Asp Phe Val Ala Phe Ser Asp Gly Tyr Asp Asp Gly
           60           65           70

CTG AAG CCC GGC GGC GAC GGG AAG CGC TAC ATG TCC GAG ATG AAA GCC      288
Leu Lys Pro Gly Gly Asp Gly Lys Arg Tyr Met Ser Glu Met Lys Ala
           75           80           85

CGC GGC TCC GAG GCC TTA AGA AAC CTC CTT CTC AAC AAC GAC GAC GTC      336
Arg Gly Ser Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn Asp Asp Val
           90           95           100

ACT TTC GTC GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG      384
Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala
    105           110           115           120
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CGT TTG TCC CAC GTC CCG ACC GCC CTT CTC TGG GTC GAG CCC GCC ACC	432
Arg Leu Ser His Val Pro Thr Ala Leu Leu Trp Val Glu Pro Ala Thr	
125 130 135	
GTG CTG TGC ATA TAC CAC TTC TAC TTC AAC GGC TAC GCA GAC GAG ATC	480
Val Leu Cys Ile Tyr His Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile	
140 145 150	
GAC GCC GGT TCC AAT GAA ATT CAG CTC CCT CGG CTT CCA TCC CTG GAG	528
Asp Ala Gly Ser Asn Glu Ile Gln Leu Pro Arg Leu Pro Ser Leu Glu	
155 160 165	
CAG CGC AGT CTT CCG ACG TTT CTG CTG CCT GCG ACG CCG GAG AGA TTC	576
Gln Arg Ser Leu Pro Thr Phe Leu Leu Pro Ala Thr Pro Glu Arg Phe	
170 175 180	
CGG TTG ATG ATG AAG GAG AAG CTG GAA ACT TTA GAC GGT GAA GAG AAG	624
Arg Leu Met Met Lys Glu Lys Leu Glu Thr Leu Asp Gly Glu Glu Lys	
185 190 195 200	
GCG AAA GTA TTG GTG AAC ACG TTT GAT GCG TTG GAG CCC GAT GCA CTC	672
Ala Lys Val Leu Val Asn Thr Phe Asp Ala Leu Glu Pro Asp Ala Leu	
205 210 215	
ACG GCT ATT GAT AGG TAT GAG TTG ATC GGG ATC GGG CCG TTG ATT CCC	720
Thr Ala Ile Asp Arg Tyr Glu Leu Ile Gly Ile Gly Pro Leu Ile Pro	
220 225 230	
TCC GCC TTC TTG GAC GGC GAA GAT CCC TCC GAA ACG TCT TAC GGC GGC	768
Ser Ala Phe Leu Asp Gly Glu Asp Pro Ser Glu Thr Ser Tyr Gly Gly	
235 240 245	
GAT CTT TTC GAA AAA TCG GAG GAG AAT AAC TGC GTG GAG TGG TTG AAC	816
Asp Leu Phe Glu Lys Ser Glu Glu Asn Asn Cys Val Glu Trp Leu Asn	
250 255 260	
TCG AAG CCG AAA TCT TCG GTG GTG TAT GTG TCG TTT GGG AGC GTT TTG	864
Ser Lys Pro Lys Ser Ser Val Val Tyr Val Ser Phe Gly Ser Val Leu	
265 270 275 280	
AGG TTT CCA AAG GCA CAA ATG GAA GAG ATT GGG AAA GGG CTA TTA GCC	912
Arg Phe Pro Lys Ala Gln Met Glu Glu Ile Gly Lys Gly Leu Leu Ala	
285 290 295	
TGC GGA AGG CCC TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC	960
Cys Gly Arg Pro Phe Leu Trp Met Ile Arg Glu Gln Lys Asn Asp Asp	
300 305 310	

0044550554460



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GGC GAA GAA GAA GAA GAA GAA GAA GAG TTG AGT TGC ATT GGG GAA TTG      1008
Gly Glu Glu Glu Glu Glu Glu Glu Glu Leu Ser Cys Ile Gly Glu Leu
      315                      320                      325

AAA AAA ATG GGG AAA ATA GTG TCG TGG TGC TCG CAG TTG GAG GTT CTG      1056
Lys Lys Met Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu
      330                      335                      340

GCG CAC CCT GCG TTG GGA TGT TTC GTG ACG CAT TGT GGG TGG AAC TCG      1104
Ala His Pro Ala Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser
      345                      350                      355                      360

GCT GTG GAG AGC TTG AGT TGC GGG ATT CCG GTG GTG GCG GTG CCG CAG      1152
Ala Val Glu Ser Leu Ser Cys Gly Ile Pro Val Val Ala Val Pro Gln
      365                      370                      375

TGG TTT GAT CAG ACG ACG AAT GCG AAG CTG ATT GAG GAT GCG TGG GGG      1200
Trp Phe Asp Gln Thr Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly
      380                      385                      390

ACA GGG GTG AGA GTG AGA ATG AAT GAA GGG GGT GGG GTT GAT GGA TGT      1248
Thr Gly Val Arg Val Arg Met Asn Glu Gly Gly Gly Val Asp Gly Cys
      395                      400                      405

GAG ATA GAA AGG TGT GTG GAG ATG GTG ATG GAT GGG GGT GAC AAG ACC      1296
Glu Ile Glu Arg Cys Val Glu Met Val Met Asp Gly Gly Asp Lys Thr
      410                      415                      420

AAA CTA GTG AGA GAA AAT GCC ATC AAA TGG AAG ACT TTG GCC AGA CAA      1344
Lys Leu Val Arg Glu Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Gln
      425                      430                      435                      440

GCC ATG GGA TAGGATGGAT CTTCACTCAA CAATCTCAAC GCCTTCTCTC      1393
Ala Met Gly
      443

GTCAAGTTGC ACACTTTTAA TCTGCTCAAA CAGCGGTTCA AATAAATATC CCCTTCCACT 1453
TAAAAAAAAA AAAAAAA
                                         1470

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Sequence ID No.: 3

Sequence length: 2062

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Verbena (Verbena hybrida)

Tissue type: Petal

Library name: cDNA library  
Clone name: pSHGT8

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Met Ser Arg Ala His Val Leu Leu Ala																	
1 5																	
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Thr	Phe	Pro	Ala	Gln	Gly	His	Ile	Asn	Pro	Ala	Leu	Gln	Phe	Ala	Lys		
10				15				20				25					
CGT	CTC	GCA	AAT	GCC	GAC	ATT	CAA	GTC	ACA	TTC	TTC	ACC	AGC	GTC	TAC	148	
Arg	Leu	Ala	Asn	Ala	Asp	Ile	Gln	Val	Thr	Phe	Phe	Thr	Ser	Val	Tyr		
30						35						40					
GCA	TGG	CGC	CGC	ATG	TCC	AGA	ACC	GCC	GCT	GGC	TCA	AAC	GGG	CTC	ATC	196	
Ala	Trp	Arg	Arg	Met	Ser	Arg	Thr	Ala	Ala	Gly	Ser	Asn	Gly	Leu	Ile		
45				50				55									
AAT	TTT	GTG	TCG	TTT	TCC	GAC	GGG	TAT	GAC	GAC	GGG	TTA	CAG	CCC	GGA	244	
Asn	Phe	Val	Ser	Phe	Ser	Asp	Gly	Tyr	Asp	Asp	Gly	Leu	Gln	Pro	Gly		
60				65				70									
GAC	GAT	GGG	AAG	AAC	TAC	ATG	TCG	GAG	ATG	AAA	AGC	AGA	GGT	ATA	AAA	292	
Asp	Asp	Gly	Lys	Asn	Tyr	Met	Ser	Glu	Met	Lys	Ser	Arg	Gly	Ile	Lys		
75				80				85									
GCC	TTG	AGC	GAT	ACT	CTT	GCA	GCC	AAT	AAT	GTC	GAT	CAA	AAA	AGC	AGC	340	
Ala	Leu	Ser	Asp	Thr	Leu	Ala	Ala	Asn	Asn	Val	Asp	Gln	Lys	Ser	Ser		
90				95				100				105					
AAA	ATC	ACG	TTC	GTG	GTG	TAC	TCC	CAC	CTC	TTT	GCA	TGG	GCG	GCC	AAG	388	
Lys	Ile	Thr	Phe	Val	Val	Tyr	Ser	His	Leu	Phe	Ala	Trp	Ala	Ala	Lys		
110						115						120					
GTG	GCG	CGT	GAG	TTC	CAT	CTC	CGG	AGC	GCG	CTA	CTC	TGG	ATT	GAG	CCA	436	
Val	Ala	Arg	Glu	Phe	His	Leu	Arg	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro		
125				130				135									
GCT	ACG	GTG	TTG	GAT	ATA	TTT	TAC	TTT	TAT	TTC	AAC	GGC	TAT	AGC	GAC	484	
Ala	Thr	Val	Leu	Asp	Ile	Phe	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ser	Asp		
140				145				150									

GAA ATC GAT GCG GGT TCG GAT GCT ATT CAC TTG CCC GGA GGA CTC CCA	532
Glu Ile Asp Ala Gly Ser Asp Ala Ile His Leu Pro Gly Gly Leu Pro	
155 160 165	
GTG CTG GCC CAG CGT GAT TTA CCG TCT TTC CTT CTT CCT TCC ACG CAT	580
Val Leu Ala Gln Arg Asp Leu Pro Ser Phe Leu Leu Pro Ser Thr His	
170 175 180 185	
GAG AGA TTC CGT TCA CTG ATG AAG GAG AAA TTG GAA ACT TTA GAA GGT	628
Glu Arg Phe Arg Ser Leu Met Lys Glu Lys Leu Glu Thr Leu Glu Gly	
190 195 200	
GAA GAA AAA CCT AAG GTC TTG GTG AAC AGC TTT GAT GCG TTG GAG CCT	676
Glu Glu Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu Glu Pro	
205 210 215	
GAT GCG CTC AAG GCC ATT GAT AAG TAC GAG ATG ATT GCA ATC GGG CCG	724
Asp Ala Leu Lys Ala Ile Asp Lys Tyr Glu Met Ile Ala Ile Gly Pro	
220 225 230	
TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAC AGG TCT	772
Leu Ile Pro Ser Ala Phe Leu Asp Gly Lys Asp Pro Ser Asp Arg Ser	
235 240 245	
TTC GGC GGA GAT TTG TTC GAG AAA GGG TCG AAT GAC GAC GAT TGC CTC	820
Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asn Asp Asp Asp Cys Leu	
250 255 260 265	
GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC	868
Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe	
270 275 280	
GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA	916
Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg	
285 290 295	
GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC	964
Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	
300 305 310	
GAA GGA GAA GAG GTA TTG ATA AGT TGC ATG GAG GAG TTG AAA CGA GTG	1012
Glu Gly Glu Glu Val Leu Ile Ser Cys Met Glu Glu Leu Lys Arg Val	
315 320 325	
GGG AAA ATT GTA TCT TGG TGT TCT CAA TTG GAA GTC CTG ACG CAT CCC	1060
Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Thr His Pro	
330 335 340 345	

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TCG TTG GGA TGT TTC GTG ACA CAC TGC GGG TGG AAT TCG ACT CTA GAG 1108
Ser Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
          350          355          360
AGT ATA TCT TTC GGG GTT CCG ATG GTG GCT TTT CCG CAG TGG TTC GAT 1156
Ser Ile Ser Phe Gly Val Pro Met Val Ala Phe Pro Gln Trp Phe Asp
          365          370          375
CAA GGG ACG AAT GCG AAG CTG ATG GAG GAT GTG TGG AGG ACG GGT GTG 1204
Gln Gly Thr Asn Ala Lys Leu Met Glu Asp Val Trp Arg Thr Gly Val
          380          385          390
AGA GTG AGA GCT AAT GAG GAG GGT AGC GTC GTT GAT GGT GAT GAA ATT 1252
Arg Val Arg Ala Asn Glu Glu Gly Ser Val Val Asp Gly Asp Glu Ile
          395          400          405
AGG AGA TGT ATT GAG GAG GTT ATG GAT GGG GGA GAA AAG AGT AGG AAA 1300
Arg Arg Cys Ile Glu Glu Val Met Asp Gly Gly Glu Lys Ser Arg Lys
          410          415          420          425
CTT AGA GAG AGT GCT GGC AAG TGG AAG GAT TTG GCA AGA AAA GCT ATG 1348
Leu Arg Glu Ser Ala Gly Lys Trp Lys Asp Leu Ala Arg Lys Ala Met
          430          435          440
GAG GAA GAT GGA TCT TCA GTT AAC AAC CTC AAG GTC TTT CTT GAT GAG 1396
Glu Glu Asp Gly Ser Ser Val Asn Asn Leu Lys Val Phe Leu Asp Glu
          445          450          455
GTT GTA GGT ATC TAAAGACGTA AATGAGGTCC CCATAGGCAA AATTGCAAAT 1448
Val Val Gly Ile
          460 461
TTCATCTCGT AAGTTGAATA CTTTTTGGCT TTAATTTTGT TCGAGTTTGT TTTTCAAAT 1508
TTATCTTGTA ATTTTACATT GAGTGTAAT TTAGTCTGAT TTAACTGGA AAAATATAAA 1568
ATTCATTGTT GAGACTCTTC ATCAAAATCA TCTGATTTCC TTTATTGTCT TGGTCAAAT 1628
TCTCATATCA ATTGGAAAAA ATAAATTTCA AAATCGTCCA ATTTTGAACC AAGAAAGAAG 1688
TATAATTTGA CCAAAATAAT AAAAGGATTC AAGTGATCTT GATGAAGTGT CTGAGCGACG 1748
AGTTCTATAT TTTTCCACCG AATTTCTAAC GAGTTTTTGA ATTTTTTTTA GCCAAAATCG 1808
GACTAACTTT GTACAAAATG AAAAGTTATA TGATGAAATT TTAAAAACA AACTCAGACA 1868
ATAATAAAGC CCCAAAGTAG TAAAATTACC TGACGAAATT TGCAATTTCC CCTCCTATTT 1928
TAATTTTTTTT GGTGTGTTTA ATAAATCGGT TATTTTACTT TTAATTAAAA TAAAAGTGAG 1988
ATGCATGATA GCTTGGTGAG TATATATGAG TTGATGGTAA TGTACGATAT TTTCTAAAAA 2048
AAAAAAAAAA AAAA 2062

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Sequence ID No.: 4

Sequence length: 1671

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Sequence type: Nucleic acid  
Number of strands: Double-strand  
Topology: Straight chain  
Source:

Biological name: Trenia

Tissue type: Petal

Direct source:

Library name: cDNA library

Clone name: pSTGT5

Sequence:

AACACATAAA AAAAAAATAA AAGAAGAAAT AATTAAAAAA AAAA ATG GTT AAC 53  
Met Val Asn  
1  
AAA CGC CAT ATT CTA CTA GCA ACA TTC CCA GCA CAA GGC CAC ATA AAC 101  
Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn  
5 10 15  
CCT TCT CTC GAG TTC GCC AAA AGG CTC CTC AAC ACC GGA TAC GTC GAC 149  
Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp  
20 25 30 35  
CAA GTC ACA TTC TTC ACG AGT GTA TAC GCA TTG AGA CGC ATG CGC TTC 197  
Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe  
40 45 50  
GAA ACC GAT CCG AGC AGC AGA ATC GAT TTC GTG GCA TKT YCA GAT TCT 245  
Glu Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser  
55 60 65  
TAC GAT GAT GGC TTA AAG AAA GGC GAC GAT GGC AAA AAC TAC ATG TCG 293  
Tyr Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn Tyr Met Ser  
70 75 80  
GAG ATG AGA AAG CGC GGA ACG AAG GCC TTA AAG GAC ACT CTT ATT AAG 341  
Glu Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr Leu Ile Lys  
85 90 95  
CTC AAC GAT GCT GCG ATG GGA AGT GAA TGT TAC AAT CGC GTG AGC TTT 389  
Leu Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg Val Ser Phe  
100 105 110 115

GTG GTG TAC TCT CAT CTA TTT TCG TGG GCA GCT GAA GTG GCG CGT GAA	437
Val Val Tyr Ser His Leu Phe Ser Trp Ala Ala Glu Val Ala Arg Glu	
120 125 130	
GTC GAC GTG CCG AGT GCC CTT CTT TGG ATT GAA CCG GCT ACG GTT TTC	485
Val Asp Val Pro Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Phe	
135 140 145	
GAT GTG TAC TAT TTT TAC TTC AAT GGG TAT GCC GAT GAT ATC GAT GCG	533
Asp Val Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Asp Ile Asp Ala	
150 155 160	
GGC TCA GAT CAA ATC CAA CTG CCC AAT CTT CCG CAG CTC TCC AAG CAA	581
Gly Ser Asp Gln Ile Gln Leu Pro Asn Leu Pro Gln Leu Ser Lys Gln	
165 170 175	
GAT CTC CCC TCT TTC CTA CTC CCT TCG AGC CCC GCG AGA TTC CGA ACC	629
Asp Leu Pro Ser Phe Leu Leu Pro Ser Ser Pro Ala Arg Phe Arg Thr	
180 185 190 195	
CTA ATG AAA GAA AAG TTC GAC ACG CTC GAC AAA GAA CCG AAA GCG AAG	677
Leu Met Lys Glu Lys Phe Asp Thr Leu Asp Lys Glu Pro Lys Ala Lys	
200 205 210	
GTC TTG ATA AAC ACG TTC GAC GCA TTA GAA ACC GAA CAA CTC AAA GCC	725
Val Leu Ile Asn Thr Phe Asp Ala Leu Glu Thr Glu Gln Leu Lys Ala	
215 220 225	
ATC GAC AGG TAT GAA CTA ATA TCC ATC GGC CCA TTA ATC CCA TCA TCG	773
Ile Asp Arg Tyr Glu Leu Ile Ser Ile Gly Pro Leu Ile Pro Ser Ser	
230 235 240	
ATA TTC TCA GAT GGC AAC GAC CCC TCA TCA AGC AAC AAA TCC TAC GGT	821
Ile Phe Ser Asp Gly Asn Asp Pro Ser Ser Ser Asn Lys Ser Tyr Gly	
245 250 255	
GGA GAC CTC TTC AGA AAA GCC GAT GAA ACT TAC ATG GAC TGG CTA AAC	869
Gly Asp Leu Phe Arg Lys Ala Asp Glu Thr Tyr Met Asp Trp Leu Asn	
260 265 270 275	
TCA AAA CCC GAA TCA TCG GTC GTT TAC GTT TCG TTC GGG AGC CTC CTG	917
Ser Lys Pro Glu Ser Ser Val Val Tyr Val Ser Phe Gly Ser Leu Leu	
280 285 290	
AGG CTC CCG AAA CCC CAA ATG GAA GAA ATA GCA ATA GGG CTT TCA GAC	965
Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly Leu Ser Asp	
295 300 305	

ACC AAA TCG CCA GTT CTC TGG GTG ATA AGA AGA AAC GAA GAG GGC GAC 1013  
Thr Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu Glu Gly Asp  
310 315 320

GAA CAA GAG CAA GCA GAA GAA GAA GAG AAG CTG CTG AGC TTC TTT GAT 1061  
Glu Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser Phe Phe Asp  
325 330 335

CGT CAC GGA ACT GAA CGA CTC GGG AAA ATC GTG ACA TGG TGC TCA CAA 1109  
Arg His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp Cys Ser Gln  
340 345 350 355

TTG GAT GTT CTG ACG CAT AAG TCG GTG GGA TGC TTC GTG ACG CAT TGC 1157  
Leu Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val Thr His Cys  
360 365 370

GGT TGG AAT TCT GCT ATC GAG AGC CTG GCT TGT GGT GTG CCC GTG GTG 1205  
Gly Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val Pro Val Val  
375 380 385

TGC TTT CCT CAA TGG TTC GAT CAA GGG ACT AAT GCG AAG ATG ATC GAA 1253  
Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Met Ile Glu  
390 395 400

GAT GTG TGG AGG AGT GGT GTG AGA GTC AGA GTG AAT GAG GAA GGC GGC 1301  
Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu Glu Gly Gly  
405 410 415

GTT GTT GAT AGG CGT GAG ATT AAG AGG TGC GTC TCG GAG GTT ATA AAG 1349  
Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu Val Ile Lys  
420 425 430 435

AGT CGA GAG TTG AGA GAA AGC GCA ATG ATG TGG AAG GGT TTG GCT AAA 1397  
Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly Leu Ala Lys  
440 445 450

GAA GCT ATG GAT GAA GAA CGT GGA TCA TCA ATG AAC AAT CTG AAG AAT 1445  
Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn Leu Lys Asn  
455 460 465

TTT ATT ACT AGG ATT ATT AAT GAA AAT GCC TCA TAAGTTGTAC 1488  
Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser  
470 475 478

TATATATGTT ATTATTGTTG TTATGGACGT CGAATTAAGT ATTAGTTAAA TGATATGTAT 1548  
TTAGAGGAAG GCCAAAACGG GCTACACCCG GCAGGCCACG GGTGGA AAAA GCCCGCCATG 1608  
ATTTAAAATA TATATTTTAA AATAAATATT TTCTACTATT AAAC TAAAAA AAAAAAAAAA 1668  
AAA 1671

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Sequence ID No.: 5  
Sequence length: 1437  
Sequence type: Nucleic acid  
Number of strands: Double-strand  
Topology: Straight chain  
Source:

Biological name: *Perilla* (*Perilla frutescens*)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p8R6

Sequence:

TTCAAACTC ATAACGTGAT TGAGCTAATG TGCACATCTT CCTCTTCAAA GTCTACAGTG 60  
TCATCCTACC AGCATCATCA TGATCAATCT CTTTATAATG AGGAGAATGG AGTAACAAGG 120  
AGTGGGTTTT GTTACTCAGC TTCAACCTAC GTACGTACTA CTACTGACTC AACTCTCAAG 180  
AGAATGAATA TAATATATAA TGGGCGATAG ATCTTTGTAG ATATGTAGGT GTAGCCTGCA 240  
GGTGGTTAAT TAATTTCCGG TGTGGGAAAA TAAATAAATA AATAAATATA GCG ATG AGC 299

Met Ser

1

AGC AGC AGC AGC AGA AGG TGG AGA GAG AAT GAG GGG ATG CGA AGG ACA 347  
Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg Thr

5

10

15

TTG CTG GGG TTG GGT TTG GGG CAG TTG GTT TCT TTC GAT TTG GCT ATC 395  
Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala Ile

20

25

30

ATG ACC TTT TCT GCT TCT TTG GTT TCA ACC ACA GTG GAT GCA CCA CTT 443  
Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro Leu

35

40

45

50

ACT ATG TCG TTC ACT ACA TAC ACT GTT GTG GCC CTG CTC TAT GGA ACC 491  
Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly Thr

55

60

65

ATC TTG CTT TAC CGC CGC CAC AAA TTC TTG GTT CCA TGG TAC TGG TAT 539  
Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr

70

75

80

Perilla frutescens



GCT CTC CTG GGG TTC GTG GAC GTC CAC GGC AAT TAT CTT GTT AAT AAA	587
Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn Lys	
85 90 95	
GCA TTC GAG TTG ACA TCG ATT ACG AGT GTG AGC ATA CTG GAT TGT TGG	635
Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys Trp	
100 105 110	
ACA ATC GTG TGG TCC ATC ATC TTT ACA TGG ATG TTC CTA GGC ACA AAA	683
Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr Lys	
115 120 125 130	
TAC TCT GTA TAC CAG TTT GTC GGT GCT GCT ATT TGT GTA GGA GGC CTC	731
Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly Leu	
135 140 145	
CTC CTC GTG CTT CTT TCC GAC TCA GGG GTC ACT GCT GCT GGT TCG AAT	779
Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser Asn	
150 155 160	
CCT CTT TTG GGT GAT TTT CTT GTC ATA ACA GGC TCT ATT TTG TTC ACA	827
Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe Thr	
165 170 175	
CTC AGC ACT GTT GGT CAG GAA TAC TGC GTG AAG AGG AAA GAT CGT ATT	875
Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg Ile	
180 185 190	
GAA GTA GTA GCA ATG ATC GGT GTA TTT GGT ATG CTC ATC AGT GCA ACC	923
Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala Thr	
195 200 205 210	
GAG ATT ACT GTG CTG GAG AGG AAT GCC CTC TCA TCA ATG CAG TGG TCT	971
Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp Ser	
215 220 225	
ACT GGA CTT TTG GCA GCC TAT GTT GTT TAT GCA CTG TCC AGC TTC CTC	1019
Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe Leu	
230 235 240	
TTC TGC ACA CTC ACC CCT TTT CTT CTC AAG ATG AGT GGC GCT GCA TTT	1067
Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala Phe	
245 250 255	
TTC AAT CTT TCC ATG CTT ACA TCT GAT ATG TGG GCT GTT GCA ATT AGG	1115
Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile Arg	
260 265 270	

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ACA TTC ATA TAC AAC CAG GAG GTT GAT TGG TTA TAC TAT TTG GCC TTT 1163  
Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala Phe  
275 280 285 290  
TGT CTC GTT GTT GTT GGA ATA TTC ATA TAT ACA AAA ACA GAG AAG GAT 1211  
Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys Asp  
295 300 305  
CCT AAC AAT ACG AGA GCC CTT GAG AAT GGA AAC TTG GAT CAT GAA TAT 1259  
Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu Tyr  
310 315 320  
AGT CTC CTT GAG GAT CAA GAT GAC ACA CCA AGA AAA CCA TAGCTAGCTT 1308  
Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro  
325 330 335  
TGCCCACAAT CTTTTCATCA ACAGTTTAA ATAATTCGTG AGGGGGAGAG AGATCGAGAT 1368  
ACTAATTAAT GGACGTCTAT TATATAGTTG GAGGTTTTTG TTTTATTAT TTATTGAGT 1428  
AAAAAAAAA 1437

Sequence ID No.: 6

Sequence length: 2105

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Petunia

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: pSPGT1

Sequence:

AGTGAGCGCA ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC 60  
TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA 120  
AACAGCTATG ACCATGATTA CGCCAAGCTC GAAATTAACC CTCACTAAAG GGAACAAAAG 180  
CTGGAGCTCC ACGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG CTGCAGGAAT 240  
TCCGTTGCTG TCGCCACAAT TTACAAACCA AGAAATTAAG CATCCCTTTC CCCCCTTAA 300  
AAAACATACA AGTTTTTAAT TTTTACTAA GCAAGAAAAT ATG GTG CAG CCT CAT GTC 358  
Met Val Gln Pro His Val

ATC TTA ACA ACA TTT CCA GCA CAA GGC CAT ATT AAT CCA GCA CTT CAA	406
Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln	
10 15 20	
TTT GCC AAG AAT CTT GTC AAG ATG GGC ATA GAA GTG ACA TTT TCT ACA	454
Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr	
25 30 35	
AGC ATT TAT GCC CAA AGC CGT ATG GAT GAA AAA TCC ATT CTT AAT GCA	502
Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala	
40 45 50	
CCA AAA GGA TTG AAT TTC ATT CCA TTT TCC GAT GGC TTT GAT GAA GGT	550
Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser Asp Gly Phe Asp Glu Gly	
55 60 65 70	
TTT GAT CAT TCA AAA GAC CCT GTA TTT TAC ATG TCA CAA CTT CGT AAA	598
Phe Asp His Ser Lys Asp Pro Val Phe Tyr Met Ser Gln Leu Arg Lys	
75 80 85	
TGT GGA AGT GAA ACT GTC AAA AAA ATA ATT CTC ACT TGC TCT GAA AAT	646
Cys Gly Ser Glu Thr Val Lys Lys Ile Ile Leu Thr Cys Ser Glu Asn	
90 95 100	
GGA CAG CCT ATA ACT TGC CTA CTT TAC TCC ATT TTC CTT CCT TGG GCA	694
Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser Ile Phe Leu Pro Trp Ala	
105 110 115	
GCA GAG GTA GCA CGT GAA GTT CAC ATC CCT TCT GCT CTT CTT TGG AGT	742
Ala Glu Val Ala Arg Glu Val His Ile Pro Ser Ala Leu Leu Trp Ser	
120 125 130	
CAA CCA GCA ACA ATA TTG GAC ATA TAT TAC TTC AAC TTT CAT GGA TAT	790
Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr Phe Asn Phe His Gly Tyr	
135 140 145 150	
GAA AAA GCT ATG GCT AAT GAA TCC AAT GAT CCA AAT TGG TCC ATT CAA	838
Glu Lys Ala Met Ala Asn Glu Ser Asn Asp Pro Asn Trp Ser Ile Gln	
155 160 165	
CTT CCC GGG CTT CCA CTA CTG GAA ACT CGA GAT CTT CCT TCA TTT TTA	886
Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg Asp Leu Pro Ser Phe Leu	
170 175 180	
CTT CCT TAT GGT GCA AAA GGG AGT CTT CGA GTT GCA CTT CCA CCA TTC	934
Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg Val Ala Leu Pro Pro Phe	
185 190 195	

AAA GAA TTG ATA GAC ACA TTA GAT GCT GAA ACC ACT CCT AAG ATT CTT	982
Lys Glu Leu Ile Asp Thr Leu Asp Ala Glu Thr Thr Pro Lys Ile Leu	
200 205 210	
GTG AAT ACA TTT GAT GAA TTA GAG CCT GAG GCA CTC AAT GCA ATT GAA	1030
Val Asn Thr Phe Asp Glu Leu Glu Pro Glu Ala Leu Asn Ala Ile Glu	
215 220 225 230	
GGT TAT AAG TTT TAT GGA ATT GGA CCG TTG ATT CCT TCT GCT TTC TTG	1078
Gly Tyr Lys Phe Tyr Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu	
235 240 245	
GGT GGA AAT GAC CCT TTA GAT GCT TCA TTT GGT GGT GAT CTT TTT CAA	1126
Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe Gly Gly Asp Leu Phe Gln	
250 255 260	
AAT TCA AAT GAC TAT ATG GAA TGG TTA AAC TCA AAG CCA AAT TCA TCA	1174
Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn Ser Lys Pro Asn Ser Ser	
265 270 275	
GTT GTT TAT ATA TCT TTT GGG AGT CTA ATG AAT CCA TCT ATT AGC CAA	1222
Val Val Tyr Ile Ser Phe Gly Ser Leu Met Asn Pro Ser Ile Ser Gln	
280 285 290	
ATG GAG GAG ATA TCA AAA GGG TTG ATA GAC ATA GGA AGG CCG TTT TTA	1270
Met Glu Glu Ile Ser Lys Gly Leu Ile Asp Ile Gly Arg Pro Phe Leu	
295 300 305 310	
TGG GTG ATA AAA GAA AAT GAA AAA GGC AAA GAA GAA GAG AAT AAA AAG	1318
Trp Val Ile Lys Glu Asn Glu Lys Gly Lys Glu Glu Glu Asn Lys Lys	
315 320 325	
CTT GGT TGT ATT GAA GAA TTG GAA AAA ATA GGA AAA ATA GTT CCA TGG	1366
Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile Gly Lys Ile Val Pro Trp	
330 335 340	
TGT TCA CAA CTT GAA GTT CTA AAA CAT CCA TCT TTA GGA TGT TTT GTT	1414
Cys Ser Gln Leu Glu Val Leu Lys His Pro Ser Leu Gly Cys Phe Val	
345 350 355	
TCT CAT TGT GGA TGG AAT TCA GCC TTA GAG AGT TTA GCT TGT GGA GTG	1462
Ser His Cys Gly Trp Asn Ser Ala Leu Glu Ser Leu Ala Cys Gly Val	
360 365 370	
CCA GTT GTG GCA TTT CCT CAA TGG ACA GAT CAA ATG ACA AAT GCC AAA	1510
Pro Val Val Ala Phe Pro Gln Trp Thr Asp Gln Met Thr Asn Ala Lys	
375 380 385 390	

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CAA GTT GAA GAT GTG TGG AAA AGT GGA GTA AGA GTG AGA ATA AAT GAA	1558
Gln Val Glu Asp Val Trp Lys Ser Gly Val Arg Val Arg Ile Asn Glu	
395 400 405	
GAT GGT GTT GTT GAA AGT GAG GAA ATC AAA AGG TGT ATT GAA TTG GTA	1606
Asp Gly Val Val Glu Ser Glu Glu Ile Lys Arg Cys Ile Glu Leu Val	
410 415 420	
ATG GAT GGA GGA GAG AAA GGG GAA GAA TTG AGA AAG AAT GCT AAG AAA	1654
Met Asp Gly Gly Glu Lys Gly Glu Glu Leu Arg Lys Asn Ala Lys Lys	
425 430 435	
TGG AAA GAA TTG GCT AGA GAA GCT GTG AAG GAA GGT GGA TCT TCA CAC	1702
Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His	
440 445 450	
AAG AAT TTA AAG GCT TTT ATT GAT GAT GTT GCC AAA GGG TTT TAATATTTAC	1754
Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe	
455 460 465 468	
AGGCTTTTGC CGTGATATTA CTTCCCCTAG TTGGCGATTC ACTCTTTGTG GACTTGCTTG	1814
ACAAAAAACT GAGGGAATGT GCTAAGACAC GCTAATGCTT TAAGAAGTCA TTTCCAAGGC	1874
TTGAAGCCTG CTTTTAAAC TTATTAGCCA GTAATCTATA GGGTTCTCTT CTATTTTCT	1934
CTGTCTCTCT TTTTAGCCTT TTTCTTTCCA AGGTTTAAGA ATAGCGTGAA CATAGCTTAG	1994
TACGTAGTCT TGGTATCTCT ATCTTACCAA GTGCAAGATT ATGCTTATGC TGTCTCCTA	2054
AATTTCTTAA TAAAATGCAA GATGAAAAAG TACAAAAAAA AAAAAAAAAA A	2105

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